

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 29, 2004, 14:05:17 ; Search time 193 Seconds
(without alignments)
80.493 Million cell updates/sec

Title: US-10-753-339-25
Perfect score: 142
Sequence: 1 KQIINWQEVGKAMYAKAFSPVPMF 27

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot 02: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	94	66.2	202	P88521	human immun
2	94	66.2	397	O11557	human immun
3	94	66.2	412	O11561	human immun
4	93	65.5	197	O74009	human immun
5	93	65.5	199	O74005	human immun
6	93	65.5	200	P88475	human immun
7	93	65.5	200	P88514	human immun
8	93	65.5	200	P88516	human immun
9	93	65.5	200	P88519	human immun
10	93	65.5	200	O73980	human immun
11	93	65.5	200	O73981	human immun
12	93	65.5	200	O74003	human immun
13	93	65.5	200	O74004	human immun
14	93	65.5	200	O9QE80	human immun
15	93	65.5	200	O9QE81	human immun
16	93	65.5	200	O9QE82	human immun
17	93	65.5	201	O73995	human immun
18	93	65.5	201	O74010	human immun
19	93	65.5	201	O9QE83	human immun
20	93	65.5	201	O9QE84	human immun
21	93	65.5	202	P88444	human immun
22	93	65.5	202	P88445	human immun
23	93	65.5	202	P88446	human immun
24	93	65.5	202	P88447	human immun
25	93	65.5	202	P88448	human immun
26	93	65.5	202	P88449	human immun
27	93	65.5	202	P88450	human immun
28	93	65.5	202	P88451	human immun
29	93	65.5	202	P88452	human immun
30	93	65.5	202	P88453	human immun
31	93	65.5	202	P88489	human immun

32	93	65.5	202	2	P88490	human immun
33	93	65.5	202	2	P88495	human immun
34	93	65.5	202	2	P88498	human immun
35	93	65.5	202	2	P88499	human immun
36	93	65.5	202	2	P88500	human immun
37	93	65.5	202	2	P88501	human immun
38	93	65.5	202	2	P88502	human immun
39	93	65.5	202	2	P88503	human immun
40	93	65.5	202	2	P88504	human immun
41	93	65.5	202	2	P88505	human immun
42	93	65.5	202	2	P88506	human immun
43	93	65.5	202	2	P88509	human immun
44	93	65.5	202	2	P88510	human immun
45	93	65.5	202	2	P88512	human immun

ALIGNMENTS

RESULT 1
P88521 PRELIMINARY; PRT; 202 AA.
AC P88521; (Tremblrel. 03, Created)
DT 01-MAY-1997 (Tremblrel. 03, Last sequence update)
DT 01-MAY-1997 (Tremblrel. 03, Last sequence update)
DE 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE Envelope glycoprotein, V3-V5 region (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97296232; PubMed=9151816;
RA Liu S.-L., Schacker T., Musey L., Shriner D., McElrath M.J., Corey L., Mullins J.I.;
RT "Divergent patterns of progression to AIDS after infection from the same source: human immunodeficiency virus type 1 evolution and antiviral responses.";
RT J. Virol. 71:4284-4295(1997).
RN [2]
RP SEQUENCE FROM N.A.
RA Liu S.-L., Shacker T., Musey L., McElrath M.J., Corey L., Mullins J.I.;
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
EMBL: U79112; AAC57411.1;
DR GO; GO:0019028; C: viral capsid; IEA.
DR GO; GO:0019031; C: viral envelope; IEA.
DR GO; GO:0005198; F: structural molecule activity; IEA.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
FT NON_TER 1
FT NON_TER 202
SQ SEQUENCE 202 AA; 22411 MW; AC257A189FE04103 CRC64;
Query Match 66.2%; Score 94; DB 2; Length 202;
Best Local Similarity 82.6%; Pred. No. 4.6e-06;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 KQIINWQEVGKAMYAKAFSPV 23
Db 146 KQIINWQEVGKAMYAPISGEV 168

RESULT 2
O11557 PRELIMINARY; PRT; 397 AA.
ID O11557
AC O11557; (Tremblrel. 04, Created)
DT 01-JUL-1997 (Tremblrel. 04, Last sequence update)
DT 01-JUL-1997 (Tremblrel. 04, Last sequence update)
DE 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	90	63.4	851	2	S33985	env polyprotein -
2	90	63.4	856	1	VCLJH3	env polyprotein pr
3	86	60.6	506	2	A40218	envelop glycoprote
4	86	60.6	854	2	S13288	env protein - huma
5	86	60.6	855	1	VCLJAZ	env polyprotein pr
6	86	60.6	856	1	VCLJVL	env polyprotein pr
7	86	60.6	859	1	VCLJMN	env polyprotein pr
8	86	60.6	861	1	VCLJLV	env polyprotein pr
9	85	59.9	290	2	S25940	env protein - huma
10	85	59.9	297	2	S60538	envelope polyprote
11	85	59.3	443	2	A41621	env polyprotein P
12	85	59.9	843	1	H44001	env polyprotein pr
13	85	59.9	847	2	T09448	envelope glycoprot
14	85	59.9	852	1	VCLJBR	env polyprotein -
15	84	59.2	445	2	A41621	env polyprotein M
16	84	59.2	454	2	B41621	env polyprotein D
17	84	59.2	729	1	VCLJXX	env polyprotein pr
18	84	59.2	861	1	VCLJSC	env polyprotein pr
19	84	59.2	861	1	VCLJKB	env polyprotein pr
20	81	57.0	847	2	S13289	env polyprotein pr
21	80.5	56.7	300	2	S60522	env protein - huma
22	80	56.3	300	2	S60522	envelope polyprote
23	80	56.3	300	2	S60547	envelope polyprote
24	80	56.3	301	2	S60548	envelope polyprote
25	79	55.6	294	2	S60525	envelope polyprote
26	79	55.6	852	2	T12016	envelope polyprote
27	79	55.6	853	2	S54384	envelope glycoprot
28	79	55.6	855	1	VCLJZR	env polyprotein pr
29	79	55.6	856	1	VCLJ3W	env polyprotein pr

env polypeptide precursor - human immunodeficiency virus type 1 (isolate HTLV-III, BH1
N;Alternate names: coat polypeptide
C;Species: human immunodeficiency virus type 1, HIV-1
A;Note: host Homo sapiens (man)
C;Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 09-Jul-2004
C;Accession: A03973
R;Ratner, L.; Haseltine, W.; Patarca, R.; Livak, K.J.; Starcich, B.; Josephs, S.F.; Do-
nberger, J.A.; Papas, T.S.; Graybe, J.; Chang, N.T.; Gallo, R.C.; Wong-Staal, F.
Nature 313, 277-284, 1985
A;Title: Complete nucleotide sequence of the AIDS virus, HTLV-III.
A;Reference number: A93353; PMID:8511123; PMID:2578615
A;Accession: A03973

A/Cross-references: UNIPROT:P03375; GB:MJ5654; GB:K02008; GB:K02009; GB:K02010; NID:93
C/Genetics:
A/Gene: env
C/Superfamily: type E retrovirus env polyprotein
C/Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polypr
F1-30/Domain: signal sequence #status predicted <SIG>
F31-51/Product: exterior membrane glycoprotein #status predicted <EXT>
F512-856/Product: transmembrane glycoprotein #status predicted <TM>
F88_136_141_156160_186_197_230_234_241_262_276_289_295_301_332_339_356_386_392_397_4
F611_616_625_637_674_750_816/Binding site: carboxyhole (Asn) (covalent) #status pred

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OM protein - protein search, using sw model

Run on: December 29, 2004, 14:37:51 ; Search time 465 Seconds
(without alignments)

64.335 Million cell updates/sec

Title: US-10-753-339-25

Perfect score: 142
Sequence: 1 KQIINWQEVGKAMKAFSEVPMF 27

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 6730630 seqs, 1107998698 residues

Total number of hits satisfying chosen parameters: 6730630

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Pending Parents AA Main.*
1: /cgn2_6/ptodata/1/paa/PCTUS COMB.pcp.*
2: /cgn2_6/ptodata/1/paa/US06 COMB.pcp.*
3: /cgn2_6/ptodata/1/paa/US07 COMB.pcp.*
4: /cgn2_6/ptodata/1/paa/US08 COMB.pcp.*
5: /cgn2_6/ptodata/1/paa/US08 COMB.pcp.*
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7: /cgn2_6/ptodata/1/paa/US08 COMB.pcp.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

*

Query Match

100.0%; Score 142; DB 1; Length 27;

Result No.	Score	Query Match	Length	DB	ID	Description
1	142	100.0	27	1	PCT-US01-03540-25	Sequence 25, Appl
2	142	100.0	27	1	PCT-US01-03540-102	Sequence 102, App
3	142	100.0	27	1	PCT-US01-03540A-25	Sequence 25, Appl
4	142	100.0	27	1	PCT-US01-03540A-102	Sequence 102, Appl
5	142	100.0	27	22	US-09-775-805-25	Sequence 25, Appl
6	142	100.0	27	22	US-09-775-805-102	Sequence 102, App
7	142	100.0	27	22	US-09-775-805A-25	Sequence 25, Appl
8	142	100.0	27	22	US-09-775-805A-102	Sequence 102, App
9	142	100.0	27	22	US-10-753-339-25	Sequence 25, Appl
10	142	100.0	27	22	US-10-753-339-102	Sequence 102, App
11	94	66.2	202	22	US-09-791-537-45937	Sequence 45937, A
12	93	65.5	197	22	US-09-791-537-86890	Sequence 86890, A
13	93	65.5	200	22	US-09-791-537-45525	Sequence 45525, A
14	93	65.5	200	22	US-09-791-537-45920	Sequence 45920, A
15	93	65.5	200	22	US-09-791-537-45923	Sequence 45923, A
16	93	65.5	200	22	US-09-791-537-45934	Sequence 45934, A
17	93	65.5	200	22	US-09-791-537-77855	Sequence 77855, A
18	93	65.5	200	22	US-09-791-537-77857	Sequence 77857, A
19	93	65.5	200	22	US-09-791-537-77860	Sequence 77860, A
20	93	65.5	200	22	US-09-791-537-86791	Sequence 86791, A
21	93	65.5	200	22	US-09-791-537-86792	Sequence 86792, A
22	93	65.5	201	22	US-09-791-537-77836	Sequence 77836, A
23	93	65.5	201	22	US-09-791-537-77852	Sequence 77852, A
24	93	65.5	201	22	US-09-791-537-135944	Sequence 135944, A
25	93	65.5	202	22	US-09-791-537-45468	Sequence 45468, A
26	93	65.5	202	22	US-09-791-537-45470	Sequence 45470, A
27	93	65.5	202	22	US-09-791-537-45471	Sequence 45471, A
28	93	65.5	202	22	US-09-791-537-45472	Sequence 45472, A
29	93	65.5	202	22	US-09-791-537-45482	Sequence 45482, A
30	93	65.5	202	22	US-09-791-537-45483	Sequence 45483, A
31	93	65.5	202	22	US-09-791-537-45484	Sequence 45484, A
32	93	65.5	202	22	US-09-791-537-45485	Sequence 45485, A
33	93	65.5	202	22	US-09-791-537-45486	Sequence 45486, A
34	93	65.5	202	22	US-09-791-537-45488	Sequence 45488, A
35	93	65.5	202	22	US-09-791-537-45489	Sequence 45489, A
36	93	65.5	202	22	US-09-791-537-45848	Sequence 45848, A
37	93	65.5	202	22	US-09-791-537-45849	Sequence 45849, A
38	93	65.5	202	22	US-09-791-537-45855	Sequence 45855, A
39	93	65.5	202	22	US-09-791-537-45870	Sequence 45870, A
40	93	65.5	202	22	US-09-791-537-45872	Sequence 45872, A
41	93	65.5	202	22	US-09-791-537-45874	Sequence 45874, A
42	93	65.5	202	22	US-09-791-537-45875	Sequence 45875, A
43	93	65.5	202	22	US-09-791-537-45878	Sequence 45878, A
44	93	65.5	202	22	US-09-791-537-45888	Sequence 45888, A
45	93	65.5	202	22	US-09-791-537-45899	Sequence 45899, A

ALIGNMENTS

RESULT 1
PCT-US01-03540-25
; Sequence 25, Application PC/TUS0103540
; GENERAL INFORMATION:
; APPLICANT: DUKE UNIVERSITY
; TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS VACCINE
; FILE REFERENCE: 1579-547
; CURRENT APPLICATION NUMBER: PCT/US01/03540
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: 09/497,497
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US01-03540-25

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OM protein - protein search, using sw model

Run on: December 29, 2004, 14:40:26 ; Search time 143 Seconds
(without alignments)
67.921 Million cell updates/sec

Title: US-10-753-339-25
Perfect score: 142
Sequence: 1 KQIINMWQEVGKAMYAKAFSPVPMF 27

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1599051 seqs, 359727711 residues
Total number of hits satisfying chosen parameters: 1599051

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
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12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	142	100.0	27	9	US-09-775-805-25
2	142	100.0	27	9	US-09-775-805-102
3	142	100.0	27	17	US-10-753-339-25
4	142	100.0	27	17	US-10-753-339-102
5	90	63.4	28	10	US-09-966-931-12
6	90	63.4	28	16	US-10-459-121-12
7	90	63.4	39	9	US-09-810-310-9
8	90	63.4	496	15	US-10-371-472-12
9	90	63.4	496	15	US-10-371-472-16
10	90	63.4	848	16	US-10-325-468-38
11	90	63.4	849	16	US-10-325-468-15
12	90	63.4	849	16	US-10-325-468-29
13	90	63.4	849	16	US-10-325-468-25

14	90	63.4	849	16	US-10-325-468-32	Sequence 32, Appl
15	90	63.4	853	13	US-10-003-035-33	Sequence 33, Appl
16	90	63.4	853	14	US-10-286-332A-33	Sequence 33, Appl
17	90	63.4	853	14	US-10-280-915-33	Sequence 33, Appl
18	90	63.4	853	16	US-10-286-332A-33	Sequence 33, Appl
19	90	63.4	855	16	US-10-325-468-25	Sequence 25, Appl
20	90	63.4	883	16	US-10-441-926-2	Sequence 2, Appl
21	90	63.4	883	16	US-10-441-949-2	Sequence 2, Appl
22	90	63.4	1101	13	US-10-003-035-53	Sequence 53, Appl
23	90	63.4	1101	14	US-10-286-332A-53	Sequence 53, Appl
24	90	63.4	1101	14	US-10-280-915-53	Sequence 53, Appl
25	90	63.4	1186	13	US-10-003-035-55	Sequence 55, Appl
26	90	63.4	1186	13	US-10-286-332A-55	Sequence 55, Appl
27	90	63.4	1186	14	US-10-280-915-55	Sequence 55, Appl
28	90	63.4	1186	14	US-10-286-332A-55	Sequence 55, Appl
29	90	63.4	1186	16	US-10-286-332A-55	Sequence 55, Appl
30	89	62.7	726	14	US-10-196-515-3	Sequence 3, Appl
31	88	62.0	25	9	US-09-775-805-29	Sequence 29, Appl
32	88	62.0	25	17	US-10-753-339-29	Sequence 29, Appl
33	88	62.0	483	15	US-10-371-472-31	Sequence 31, Appl
34	88	62.0	487	15	US-10-371-472-33	Sequence 33, Appl
35	88	62.0	498	15	US-10-371-472-5	Sequence 5, Appl
36	87	61.3	236	10	US-09-827-688-2	Sequence 2, Appl
37	86	60.6	28	10	US-09-966-931-4	Sequence 4, Appl
38	86	60.6	28	10	US-09-966-931-5	Sequence 5, Appl
39	86	60.6	28	10	US-09-966-931-10	Sequence 10, Appl
40	86	60.6	28	10	US-09-966-931-11	Sequence 11, Appl
41	86	60.6	28	10	US-09-966-931-13	Sequence 13, Appl
42	86	60.6	28	10	US-09-966-931-15	Sequence 15, Appl
43	86	60.6	28	10	US-09-966-931-21	Sequence 21, Appl
44	86	60.6	28	14	US-10-105-545-14	Sequence 14, Appl
45	86	60.6	28	16	US-10-459-121-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1
US-09-775-805-25
; Sequence 25, Application US/09775805
; Publication No. US20010036461A1
; GENERAL INFORMATION:
; APPLICANT: DUKE UNIVERSITY
; TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS VACCINE
; FILE REFERENCE: 1579-548
; CURRENT APPLICATION NUMBER: US/09/775,805
; CURRENT FILING DATE: 2001-02-05
; PRIOR FILING DATE: 09/497,497
; PRIOR APPLICATION NUMBER: 2000-02-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-775-805-25

Query Match 100.0%; Score 142; DB 9; Length 27;
Best Local Similarity 100.0%; Pred. No. 2,1e-14;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KQIINMWQEVGKAMYAKAFSPVPMF 27
DB 1 KQIINMWQEVGKAMYAKAFSPVPMF 27

RESULT 2
US-09-775-805-102
; Sequence 102, Application US/09775805
; Publication No. US20010036461A1
; GENERAL INFORMATION:
; APPLICANT: DUKE UNIVERSITY
; TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS VACCINE

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 29, 2004, 14:31:10 ; Search time 38 seconds
(without alignments)
47.121 Million cell updates/sec

Title: US-10-753-339-25

Perfect score: 142

Sequence: 1 KQIINWQEVGKMYAKAFSPVIMPF 27

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

1: /cgn2_6/prodata/1/iaa/5A COMB.pep:*

2: /cgn2_6/prodata/1/iaa/5B COMB.pep:*

3: /cgn2_6/prodata/1/iaa/6A COMB.pep:*

4: /cgn2_6/prodata/1/iaa/6B COMB.pep:*

5: /cgn2_6/prodata/1/iaa/PCTUS COMB.pep:*

6: /cgn2_6/prodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	90	63.4	24	2	US-08-455-625-24
2	90	63.4	24	3	Sequence 24, Appl
3	90	63.4	24	3	Sequence 3, Appl
4	90	63.4	24	3	Sequence 24, Appl
5	90	63.4	24	3	Sequence 24, Appl
6	90	63.4	24	5	US-08-060-988A-24
7	90	63.4	24	5	US-09-508-552-18
8	90	63.4	28	1	PCT-US94-05142-24
9	90	63.4	28	2	US-08-488-252-1
10	90	63.4	28	3	US-08-448-603A-12
11	90	63.4	28	3	US-09-134-075-12
12	90	63.4	28	5	US-09-492-739-12
13	90	63.4	39	2	PCT-US92-06688-1
14	90	63.4	39	2	US-08-455-625-2
15	90	63.4	39	3	US-08-455-685-2
16	90	63.4	39	3	US-08-455-685-2
17	90	63.4	39	3	US-08-060-988A-2
18	90	63.4	39	4	US-08-060-988A-28
19	90	63.4	39	4	US-09-508-552-2
20	90	63.4	39	5	US-09-508-552-9
21	90	63.4	39	5	PCT-US94-05142-2
22	90	63.4	39	5	PCT-US94-05142-28
23	90	63.4	181	5	PCT-US93-07805-1
24	90	63.4	496	3	US-08-889-841B-12
25	90	63.4	496	3	US-08-889-841B-16
26	90	63.4	496	4	US-09-419-362-12
27	90	63.4	496	4	US-09-419-362-16
28	90	63.4	856	3	US-09-124-900-9

28 90 63.4 863 3 US-08-463-210-11 Sequence 11, Appl

29 90 63.4 863 4 US-08-463-028-11 Sequence 11, Appl

30 90 63.4 880 2 US-08-788-815-7 Sequence 7, Appl

31 90 63.4 880 3 US-09-157-963-7 Sequence 7, Appl

32 90 63.4 880 4 US-09-568-105-7 Sequence 7, Appl

33 89 62.7 28 1 US-08-488-252-7 Sequence 7, Appl

34 89 62.7 62 1 US-08-105-483-444 Sequence 444, App

35 89 62.7 62 1 US-08-709-209-444 Sequence 444, App

36 89 62.7 62 1 US-08-303-275-155 Sequence 155, App

37 89 62.7 62 1 US-08-458-101-444 Sequence 444, App

38 89 62.7 519 3 US-08-472-240A-18 Sequence 18, Appl

39 89 62.7 726 4 US-09-337-387-3 Sequence 3, Appl

40 89 62.7 865 3 US-07-956-483-13 Sequence 13, Appl

41 89 62.7 887 3 US-08-472-240A-4 Sequence 4, Appl

42 88 62.0 483 3 US-08-889-841B-31 Sequence 31, Appl

43 88 62.0 483 4 US-09-419-362-31 Sequence 31, Appl

44 88 62.0 487 3 US-08-889-841B-33 Sequence 33, Appl

45 88 62.0 487 4 US-09-419-362-33 Sequence 33, Appl

ALIGNMENTS

RESULT 1

US-08-455-625-24

Sequence 24, Application US/08455625

Patent No. 5932218

GENERAL INFORMATION:

APPLICANT: Berzofsky, Jay A.

APPLICANT: Ahlers, Jeffrey D.

APPLICANT: Pendleton, C. D.

APPLICANT: Nara, Peter

APPLICANT: Shirai, Mutsunori

TITLE OF INVENTION: COMPOSITE SYNTHETIC PEPTIDE CONSTRUCT

TITLE OF INVENTION: ELICITING NEUTRALIZING ANTIBODIES AND CYTOTOXIC T

TITLE OF INVENTION: LYMPHOCYTES AGAINST HIV

NUMBER OF SEQUENCES: 36

CORRESPONDENCE ADDRESS:

ADDRESSEE: Birch, Stewart, Kolasch & Birch

STREET: P.O. Box 747

CITY: Falls Church

STATE: Virginia

COUNTRY: USA

ZIP: 22040-0747

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/455,625

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/060,988

FILING DATE: 14-MAY-1993

ATTORNEY/AGENT INFORMATION:

NAME: Svensson, Leonard R.

REGISTRATION NUMBER: 30330

REFERENCE/DOCKET NUMBER: 1173-434P

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-205-8000

TELEFAX: 703-205-8050

INFORMATION FOR SEQ ID NO: 24:

SEQUENCE CHARACTERISTICS:

LENGTH: 24 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

FRAGMENT TYPE: internal

FEATURE:

NAME/KEY: Peptide

LOCATION: 1..24

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 29, 2004, 14:03:20 ; Search time 159 Seconds
(without alignments)
60.916 Million cell updates/sec

Title: US-10-753-339-25

Perfect score: 142

Sequence: 1 KQIINWQEVGKAMYAKAFSPVPMF 27

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_23Sep04:*

1: Geneseq1980s:*

2: Geneseq1990s:*

3: Geneseq2000s:*

4: Geneseq2001s:*

5: Geneseq2002s:*

6: Geneseq2003as:*

7: Geneseq2003bs:*

8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	142	100.0	27	4	AAU12476 HIV Th-CT
2	142	100.0	27	4	AAU12553 Human HIV
3	142	100.0	27	5	AAU70239 HIV Th-CT
4	142	100.0	27	5	AAU70264 HIV gag T
5	142	100.0	137	5	AAU10481 HIV Th-CT
6	90	63.4	24	2	AAE33837 Cluster P
7	90	63.4	24	2	AAE66431 HIV-1 CLU
8	90	63.4	24	2	AAE66431 HIV-1 CLU
9	90	63.4	24	6	ABG71784 HIV-1 non
10	90	63.4	25	1	AAU71144 Anti-HIV
11	90	63.4	25	1	AAU80749 Sequence
12	90	63.4	28	2	AAU54909 HIV gp120
13	90	63.4	32	2	AAU76910 Fusion Im
14	90	63.4	39	2	AAE66409 PCLUS 3-1
15	90	63.4	39	2	AAE66435 PCLUS 3-1
16	90	63.4	39	2	AAU05346 HIV-1 CLU
17	90	63.4	39	2	AAU05339 HIV-1 CLU
18	90	63.4	39	4	AAE07857 Synthetic
19	90	63.4	39	5	ABG68641 HIV-1 gp1
20	90	63.4	39	5	ABG68648 HIV-1 gp1
21	90	63.4	68	2	AAU7845 HIV gp120
22	90	63.4	117	5	AAU10478 HIV/Mouse
23	90	63.4	178	2	AAE22564 Antibody
24	90	63.4	179	1	AAU93537 HIV porti
25	90	63.4	179	1	AAU92014 HIV porti

26	90	63.4	180	4	AAG78506 Recombina
27	90	63.4	181	2	AAR49610 HIV-1 gp1
28	90	63.4	234	1	AAP81143 Sequence
29	90	63.4	234	1	AAP92010 HTLV-III
30	90	63.4	234	2	AAR31943 Recombina
31	90	63.4	234	1	AAP71198 Sequence
32	90	63.4	319	1	AAP71199 Sequence
33	90	63.4	353	1	AAP92015 HIV porti
34	90	63.4	423	1	AAP93536 Sequence
35	90	63.4	423	1	AAP92013 Sequence
36	90	63.4	496	2	AAR37058 HIV-1 bre
37	90	63.4	496	2	AAR37059 HIV-1 bre
38	90	63.4	496	8	ADK19351 HIV DNA g
39	90	63.4	496	8	ADK19354 HIV DNA g
40	90	63.4	500	7	AAE39549 HIV gp120
41	90	63.4	504	7	AAE39547 HIV gp120
42	90	63.4	511	6	ABRS5435 Amino aci
43	90	63.4	597	1	AAP93539 HIV porti
44	90	63.4	640	1	AAP92012 HTLV-III
45	90	63.4	819	1	AAP81144 Sequence

ALIGNMENTS

RESULT 1
AAU12476

ID AAU12476 standard; peptide; 27 AA.

XX AC AAU12476;

DT 27-SEP-2001 (first entry)

XX XX HIV Th-CTL peptide prototype vaccine immunogen #13.

XX KW Human immunodeficiency virus; HIV; immunogen; vaccine; anti-HIV;
KW human leukocyte antigen; HLA; T-helper epitope; CTL; Th; epitope;
KW major histocompatibility complex; MHC; cytotoxic T-lymphocyte;
KW Vaccinia ankara.

XX OS Homo sapiens.

XX PN WQ200156355-A2.

XX PD 09-AUG-2001.

XX PF 05-FEB-2001; 2001WO-US003540.

XX PR 04-FEB-2000; 2000US-00497497.

XX PA (UYDU-) UNIV DUKE.

XX PI Haynes BF, Liao H;

XX XX WPI; 2001-489827/53.

PT Vaccine for immunizing against human immunodeficiency virus has mixture
PT or linear array of peptides comprising immunodominant T-helper epitopes
PT and major histocompatibility complex cytotoxic T-lymphocyte epitopes.

PS Claim 1; Page 24; 33pp; English.

CC The present invention relates to human immunodeficiency virus (HIV) and
CC in particular to a human leukocyte antigen (HLA)-based HIV vaccine. The
CC vaccine comprises a mixture or linear array of peptides, or its variants,
CC where the peptides contain immunodominant T-helper (Th) epitopes and
CC major histocompatibility complex (MHC) cytotoxic T-lymphocyte (CTL)
CC epitopes and the linear array of peptides are preferably expressed in
CC modified Vaccinia ankara. The vaccine is useful for immunising a patient
CC against HIV and focuses immune response on many dominant and subdominant
CC CTL epitopes of HIV. DNA or live vectors with linear arrays of CTL
CC epitopes can be used as either primes or boosts of peptides or of each
CC other to optimally give CTL anti-HIV responses. The vaccine induces